

#3



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,348

DATE: 01/19/2002
TIME: 11:38:41

Input Set : A:\18176seq.txt
Output Set: N:\CRF3\01192002\J019348.raw

p.5

3 <110> APPLICANT: Nelson, Peter S
4 Hood, Leroy
5 Lin, Biaoyang
7 <120> TITLE OF INVENTION: Prostate-Specific Nucleic Acids
9 <130> FILE REFERENCE: UO FW-1-18176
11 <140> CURRENT APPLICATION NUMBER: US/10/019,348
12 <141> CURRENT FILING DATE: 2001-10-22
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/10920
15 <151> PRIOR FILING DATE: 2000-04-21
17 <150> PRIOR APPLICATION NUMBER: 60/130,778
18 <151> PRIOR FILING DATE: 1999-04-23
20 <150> PRIOR APPLICATION NUMBER: 60/151,585
21 <151> PRIOR FILING DATE: 1999-08-30
23 <150> PRIOR APPLICATION NUMBER: 60/174,003
24 <151> PRIOR FILING DATE: 1999-12-30
26 <150> PRIOR APPLICATION NUMBER: 60/177,751
27 <151> PRIOR FILING DATE: 2000-01-24
29 <160> NUMBER OF SEQ ID NOS: 42
31 <170> SOFTWARE: PatentIn Ver. 2.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2538
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (53)..(994)
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44 Met Phe
45 1
47 ccg ctg ttg ctc ctc ctt ctg ccc ttc ctt ctg tat atg gct gcg ccc 106
48 Pro Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro
49 5 10 15
51 caa atc agg aaa atg ctg tcc agt ggg gtg tgt aca tca act gtt cag 154
52 Gln Ile Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln
53 20 25 30
55 ctt cct ggg aaa gta gtt gtg gtc aca gga gct aat aca ggt atc ggg 202
56 Leu Pro Gly Lys Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly
57 35 40 45 50
59 aag gag aca gcc aaa gag ctg gct cag aga gga gct cga gta tat tta 250
60 Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Leu
61 55 60 65
63 gct tgc cgg gat gtg gaa aag ggg gaa ttg gtg gcc aaa gag atc cag 298

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64 Ala Cys Arg Asp Val Glu Lys Gly Glu Leu Val Ala Lys Glu Ile Gln			
65 70	75	80	
67 acc acg aca ggg aac cag cag gtg ttg gtg cgg aaa ctg gac ctg tct			346
68 Thr Thr Thr Gly Asn Gln Gln Val Leu Val Arg Lys Leu Asp Leu Ser			
69 85	90	95	
71 gat act aag tct att cga gct ttt gct aag ggc ttc tta gct gag gaa			394
72 Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Leu Ala Glu Glu			
73 100	105	110	
75 aag cac ctc cac gtt ttg atc aac aat gca gga gtg atg atg tgt ccg			442
76 Lys His Leu His Val Leu Ile Asn Asn Ala Gly Val Met Met Cys Pro			
77 115	120	125	130
79 tac tcg aag aca gca gat ggc ttt gag atg cac ata gga gtc aac cac			490
80 Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val Asn His			
81 135	140	145	
83 ttg ggt cac ttc ctc cta acc cat ctg ctg cta gag aaa cta aag gaa			538
84 Leu Gly His Phe Leu Leu Thr His Leu Leu Leu Glu Lys Leu Lys Glu			
85 150	155	160	
87 tca gcc cca tca agg ata gta aat gtg tct tcc ctc gca cat cac ctg			586
88 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His His Leu			
89 165	170	175	
91 gga agg atc cac ttc cat aac ctg cag ggc gag aaa ttc tac aat gca			634
92 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala			
93 180	185	190	
95 ggc ctg gcc tac tgt cac agc aag cta gcc aac atc ctc ttc acc cag			682
96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln			
97 195	200	205	210
99 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta			730
100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val			
101 215	220	225	
103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct ttc atg			778
104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met			
105 230	235	240	
107 aga tgg atg tgg tgg ctt tcc ttt ttc atc aag act cct cag cag			826
108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln			
109 245	250	255	
111 gga gcc cag acc agc ctg cac tgt gcc tta aca gaa ggt ctt gag att			874
112 Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu Glu Ile			
113 260	265	270	
115 cta agt ggg aat cat ttc agt gac tgt cat gtg gca tgg gtg tct gtc			922
116 Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val Ser Val			
117 275	280	285	290
119 caa gct cgt aat gag act ata gca agg cgg ctg tgg gac gtc agt tgt			970
120 Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val Ser Cys			
121 295	300	305	
123 gac ctg ctg ggc ctc cca ata gac taacaggcag tgccagttgg acccaagaga			1024
124 Asp Leu Leu Gly Leu Pro Ile Asp			
125 310			
127 agactgcagc agactacaca gtacttcttg tcaaatgat tctccttcaa ggttttcaaa			1084
129 accttttagca caaagagagc aaaaccttcc agccttgctc gcttgggtc cagttaaaac			1144

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131 tcagtgtact gccagattcg tctaaatgtc tgtcatgtcc agatttactt tgcttctgtt 1204
133 actgccagag ttactagaga tatacataata ggataagaag accctcatat gacctgcaca 1264
135 gtcattttc cttctgaaag aaactactac cttaggagaat ctaagctata gcagggatga 1324
137 tttatgcaaa tttgaactag cttctttgtt cacaattcag ttcctccaa ccaaccagtc 1384
139 ttcacttcaa gagggccaca ctgcaaccc tcgatggatc accggaggc agtagttcaa gaccagcctg 1444
141 ggagcagggc ttgcccaggc atgggtggatc accggaggc agtagttcaa gaccagcctg 1504
143 gccaacatgg tgaaaacccca cctctactaa aaattgtgt tatctttgtg tgtcttcctg 1564
145 tttatgtgtg ccaagggagt attttcacaa agttcaaaac agccacaata atcagagatg 1624
147 gagcaaacca gtgcacatcca gtctttatgc aaatgaaatg ctgcaaaggg aagcagattc 1684
149 tgtatatgtt ggttaactacc caccaagagc acatgggtg cagggaaagaa gtaaaaaaaag 1744
151 agaaggagaa tactggaaga taatgcacaa aatgaaggga ctatgtttaagg attaacttagc 1804
153 ctttaagga ttaacttagtt aaggattaaat agcaaaagat attaaatatg ctaacatagc 1864
155 tatggaggaa ttgagggcaa gcacccagga ctgtatgaggt cttacaacaaa accagtgtgg 1924
157 caaaaaaaaaaaaaaaa aaaaaaaaaaaa atccaaaaaa caaacaaaca aaaaaaaaaa 1984
159 ttcttcattt agaaaaattt tcttagggac tgatattggt aattatggc aatttaataa 2044
161 tattttgggg catttcctt cattgtctg acaagattaa aatgtctgtg ccaaaaatttt 2104
163 gtattttattt tggagacttc ttatcaaaag taatgctgcc aaaggaagtc taaggaatta 2164
165 gtatgttcc catcaacttgt ttggagtgtg ctattctaaa agatttgtat ttcctggaat 2224
167 gacaattata ttttaacttt ggtggggaa agagttatag gaccacagtc ttcacttctg 2284
169 atacttgtaa attaatcttt tattgcactt gtttgacca ttaagctata tgtttagaaa 2344
171 tggtcattttt acggaaaaat tagaaaaattt ctgataatag tgcagaataa atgaattaat 2404
173 gttttactta atttatattt aactgtcaat gacaaataaa aattctttt gattattttt 2464
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181 <211> LENGTH: 314
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
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187 1 5 10 15
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189 20 25 30
190 Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly Ala Asn Thr Gly
191 35 40 45
192 Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val
193 50 55 60
194 Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu Val Ala Lys Glu
195 65 70 75 80
196 Ile Gln Thr Thr Gly Asn Gln Gln Val Leu Val Arg Lys Leu Asp
197 85 90 95
198 Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Leu Ala
199 100 105 110
200 Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala Gly Val Met Met
201 115 120 125
202 Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val
203 130 135 140
204 Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu Leu Glu Lys Leu
205 145 150 155 160

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216 Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His
217 165 170 175
219 His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr
220 180 185 190
222 Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe
223 195 200 205
225 Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr
226 210 215 220
228 Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser
229 225 230 235 240
231 Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro
232 245 250 255
234 Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu
235 260 265 270
237 Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val
238 275 280 285
240 Ser Val Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val
241 290 295 300
243 Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
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249 <212> TYPE: DNA
250 <213> ORGANISM: Homo sapiens
252 <220> FEATURE:
253 <221> NAME/KEY: CDS
254 <222> LOCATION: (57)..(1535)
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258 1 Met
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261 gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac 107
262 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
263 5 10 15
265 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc 155
266 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
267 20 25 30
269 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg 203
270 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Pro Ser Pro Val
271 35 40 45
273 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc 251
274 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
275 50 55 60 65
277 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act 299
278 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
279 70 75 80
281 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga 347
282 Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
283 85 90 95

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285	gct	gcg	ctg	gcc	gct	ggc	cta	ctc	tgg	aag	ttc	atg	ggc	agc	aag	tgc	395
286	Ala	Ala	Leu	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys	Cys		
287	100														110		
289	tcc	aac	tct	ggg	ata	gag	tgc	gac	tcc	tca	ggt	acc	tgc	atc	aac	ccc	443
290	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	Pro	
291	115														125		
293	tct	aac	tgg	tgt	gat	ggc	gtg	tca	cac	tgc	ccc	ggc	ggg	gag	gac	gag	491
294	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	Glu	
295	130														145		
297	aat	cgg	tgt	gtt	cgc	ctc	tac	gga	cca	aac	ttc	atc	ctt	cag	atg	tac	539
298	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met	Tyr	
299	150														160		
301	tca	tct	cag	agg	aag	tcc	tgg	cac	cct	gtg	tgc	caa	gac	gac	tgg	aac	587
302	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp	Asn	
303	165														175		
305	gag	aac	tac	ggg	cgg	gcg	gcc	tgc	agg	gac	atg	ggc	tat	aag	aat	aat	635
306	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn	Asn	
307	180														190		
309	ttt	tac	tct	agc	caa	gga	ata	gtg	gat	gac	agc	gga	tcc	acc	agc	ttt	683
310	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	Phe	
311	195														205		
313	atg	aaa	ctg	aac	aca	agt	gcc	ggc	aat	gtc	gat	atc	tat	aaa	aaa	ctg	731
314	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Leu		
315	210														225		
317	tac	cac	agt	gat	gcc	tgt	tct	tca	aaa	gca	gtg	gtt	tct	tta	cgc	tgt	779
318	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg	Cys	
319	230														240		
321	tta	gcc	tgc	ggg	gtc	aac	ttg	aac	tca	agc	cgc	cag	agc	agg	atc	gtg	827
322	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile	Val	
323	245														255		
325	ggc	ggt	gag	agc	gcg	ctc	ccg	ggg	gcc	tgg	ccc	tgg	cag	gtc	agc	ctg	875
326	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	Leu	
327	260														270		
329	cac	gtc	cag	aac	gtc	cac	gtg	tgc	gga	ggc	tcc	atc	atc	acc	ccc	gag	923
330	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	Glu	
331	275														285		
333	tgg	atc	gtg	aca	gcc	ggc	cac	tgc	gtg	gaa	aaa	cct	ctt	aat	cca		971
334	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	Pro	
335	290														305		
337	tgg	cat	tgg	acg	gca	ttt	gct	ggg	att	ttg	aga	caa	tct	ttc	atg	ttc	1019
338	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met	Phe	
339	310														320		
341	tat	gga	gcc	gga	tac	caa	gta	caa	aaa	gtg	att	tct	cat	cca	aat	tat	1067
342	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn	Tyr	
343	325														335		
345	gac	tcc	aag	acc	aag	aac	aat	gac	att	gct	ctg	atg	aag	ctg	cag	aag	1115
346	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Lys	
347	340														350		
349	cct	ctg	act	ttc	aac	gac	cta	gtg	aaa	cca	gtg	tgt	ctg	ccc	aac	cca	1163

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/019,348

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Input Set : A:\18176seq.txt
Output Set: N:\CRF3\01192002\J019348.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20